

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L., et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

09876348.060701

- (2) INFORMATION FOR SEQ. ID NO: 1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Peptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) FRAGMENT TYPE: N-terminal fragment
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
 - (ix) FEATURES:
 - (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
 1 5 10 15

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(2) INFORMATION FOR SEQ. ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC      36
                               Met Lys Leu Leu
                               -15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG      81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu
-10                               -5                               1

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT      126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
5                               10                               15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC      171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
20                               25                               30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT      216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
35                               40                               45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG      261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val
50                               55                               60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC      306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn
65                               70                               75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA      351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg
80                               85                               90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG      396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met
95                               100                               105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA      439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
110                               115

CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAA AAAGTGTTTC      489

TGATGTAATAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTTAGAG      539

CGGCCGCGGG CCCATCGTTT TCCACCC      566

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(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
  -15                      -10                      -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
   1                      5                      10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
  15                      20                      25                      30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
   35                      40                      45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
   50                      55                      60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
   65                      70                      75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
   80                      85                      90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro
   95                      100                      105                      110

Lys Phe Ser Pro Val Asp *
  115

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(2) INFORMATION FOR SEQ. ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
 1             5             10             15
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
      20             25             30
Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
      35             40             45
Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
      50             55             60
Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
      65             70             75             80
Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
      85             90             95
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
      100            105            110
Ser Pro Val Asp *
      115

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09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 5
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: c.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15	-10
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5	1
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10	15
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25	30
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40	45
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55	60
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70	75
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85	90
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100	105
ATT GAT TAA TTGTTTGTG TTTGACTGAA TTTTGACAAT AAAGGTAATA	455
Ile Asp *	
115	
TCGTTATGTA AAAAAAAAAA AAAAAA	481

- (2) INFORMATION FOR SEQ. ID NO: 6
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
      -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Lys Ile Val
      70                      75      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105      110

ATT GAT TAA TTGTTTGTG TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGAA AAAAAAAAAA AAAAAAA      482

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(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
  1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
  15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
  35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
  50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
  65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
  80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
  95                      100                      105                      110

Phe Ser Pro Ile Asp *
  115

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09076348.060701

(2) INFORMATION FOR SEQ. ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1 5 10 15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35 40 45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50 55 60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85 90 95

Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100 105 110

Pro Ile Asp *

- (2) INFORMATION FOR SEQ. ID NO: 9
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
      -15                               -10

ATC  GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                               1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                               15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                               30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                               45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                               60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                               75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                               90 95

GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                              105 110

ATT GAT TAA TTGTTTGTGTTTACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

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- (2) INFORMATION FOR SEQ. ID NO: 10
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Clone 3.4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
    -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
    35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
    50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
    65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
    80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
    95                      100                      105                      110

Phe Ser Pro Ile Asp *
    115

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- (2) INFORMATION FOR SEQ. ID NO: 11
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein for Clone 3.4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 1             5             10             15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
      20             25             30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
      35             40             45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
      50             55             60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
      65             70             75             80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
      85             90             95

Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
      100             105             110

Pro Ile Asp *
      115

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- (2) INFORMATION FOR SEQ. ID NO: 12
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser	
10	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly	
40	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100	
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA	455
Ile Asp *	
115	
TCGTTATGAA AAAAAAAAAA AAAAAAA	482

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- (2) INFORMATION FOR SEQ. ID NO: 13
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
- (ix) FEATURES
- (D) OTHER INFORMATION: Precursor Protein for Clone 3.9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
   1                      5                      10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
  15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
  35                      40                      45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
  50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
  65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
  80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
  95                      100                      105                      110

Phe Ser Pro Ile Asp *
  115

```

09070346.060701

(2) INFORMATION FOR SEQ. ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Mature protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 1          5          10          15
Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
 20          25          30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
 35          40          45
Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
 50          55          60
Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu Val Asp
 65          70          75          80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
 85          90          95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100        105        110
Pro Ile Asp *
      115

```

00076348-060701

(2) INFORMATION FOR SEQ. ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	90
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTGCGCTGAA TTTTGACAAT AAAGGTACTA	455
Ile Asp *	
115	
TCGTTATGTA AAAAAAAAAA AAAAAA	481

09076348.060701

- (2) INFORMATION FOR SEQ. ID NO: 16
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTATAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Gln Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 5 10	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCCTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

09876348.060701

- (2) INFORMATION FOR SEQ. ID NO: 17
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -55                      -50                      -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -40                      -35                      -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
      -25                      -20                      -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
      -10                      -5                      1                      5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
      10                      15                      20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
      40                      45                      50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
      55                      60                      65                      70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
      75                      80                      85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
      90                      95                      100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                      110                      115

```

09676348-060701

- (2) INFORMATION FOR SEQ. ID NO: 18
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 543 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.2
 (ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, signal minus
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50
 AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96
 Met Gly Ser Ser His His His His His Ser
 -30 -25
 AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
 Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
 -20 -15
 GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186
 Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln
 -5 1 5
 AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231
 Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20
 TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT 276
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp
 25 30 35
 GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321
 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr
 40 45 50
 GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366
 Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
 55 60 65
 GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411
 Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
 70 75 80
 GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
 85 90 95
 TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110
 CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543
 Pro Ile Asp *
 115



(2) INFORMATION FOR SEQ. ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
     15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
      95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

```

F02690-84E92860

- (2) INFORMATION FOR SEQ. ID NO: 20
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal Plus

09876348.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTATAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTAATTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 5 10	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

09076348-060701

- (2) INFORMATION FOR SEQ. ID NO: 21
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -55                               -50                       -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -40                               -35                       -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
      -25                               -20                       -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
      -10                               -5                        1              5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
      10                               15                       20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                               30                       35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
      40                               45                       50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
      55                               60                       65                       70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
      75                               80                       85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
      90                               95                       100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                               110                       115

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09076348-060701

- (2) INFORMATION FOR SEQ. ID NO: 22
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGG CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGG GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
      15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
      95                      100                      105                      110

Phe Ser Pro Ile Asp *
      115

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09876348.060701

- (2) INFORMATION FOR SEQ. ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -65 -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -50 -45 -40	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser -20 -15 -10	231
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile -5 1 5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15 20	321
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	456
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp 75 Asn Asp Glu Glu Thr Glu 70 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 90 95	546
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105 110	595
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAATGG Phe Ser Pro Val Asp * 115	643
TGTGCTTTAC ATATAAAAAA AAAGTGTTTC TGATGTAAAA AAAAAAAAAA	693
AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

09876543210

- (2) INFORMATION FOR SEQ. ID NO: 25
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                               -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                               -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
   -25                               -20                               -15                               -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
   -5                               1                               5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
   10                               15                               20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
   25                               30                               35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
   40                               45                               50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
   55                               60                               65                               70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
   75                               80                               85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
   90                               95                               100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
   105                               110                               115

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090716348-060701

- (2) INFORMATION FOR SEQ. ID NO: 26
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
- (B) CLONE: 13.17
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGG CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

RB125 RT

- (2) INFORMATION FOR SEQ. ID NO: 28
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGG CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 -5 10	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGG GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

D676348-060701

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 173 Amino Acids
    (B) TYPE: Amino Acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Protein
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: cDNA
    (B) CLONE: 3.4
(ix) FEATURES
    (D) OTHER INFORMATION: Precursor protein with His-tag
(x) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

```
Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                      110                      115
```

- (2) INFORMATION FOR SEQ. ID NO: 30
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	76
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Val Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

RB125 RT

- (2) INFORMATION FOR SEQ. ID NO: 32
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTA6CGG ATGGAATTC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 5 10	276
AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACT GAGCACCACC ACCACCACCA CTGAGAT	682

09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 33
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                   -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                   -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                   -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
   -10                               -5                      1          5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
   10                               15                   20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                   35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val
   40                               45                   50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                   65                   70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                   85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                   100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
   105                               110                   115

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09076748.050701

- (2) INFORMATION FOR SEQ. ID NO: 34
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
      15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
      95                      100                      105                      110

Phe Ser Pro Ile Asp *
      115

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09076348-060701

- (2) INFORMATION FOR SEQ. ID NO: 36
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 5 10	276
AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGCGTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

00076346-060701

- (2) INFORMATION FOR SEQ. ID NO: 37
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
      -55                      -50                      -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -40                      -35                      -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
      -25                      -20                      -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
      -10                      -5                      1                      5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
      10                      15                      20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
      40                      45                      50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
      55                      60                      65                      70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
      75                      80                      85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
      90                      95                      100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                      110                      115

```

00076348.060701

- (2) INFORMATION FOR SEQ. ID NO: 38
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

- (2) INFORMATION FOR SEQ. ID NO: 39
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Mature protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
      15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
      95                      100                      105                      110

Phe Ser Pro Ile Asp *
      115

```

09075348-060704

- (2) INFORMATION FOR SEQ. ID NO: 40
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG 24

09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 41
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 42
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
- CGCGGATCCC TGACCGAGGC ACAA 24

09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 43
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAAC TGAGC TCGCC 25

09075348-060701

- (2) INFORMATION FOR SEQ. ID NO: 44
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 2-2
- (ix) FEATURES
- (B) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGC	CAG	GAC	AAA	ATG	AAA	CTC	CTC	TTG	TGC	TTT	GCN	TTC	GCC	GCC	46
				Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala	
								-15						-10	
ATC	GTC	ATC	GGA	GCT	CAG	GCT	CTC	ACC	GAY	GAA	CAG	ATA	CAG	AAA	91
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	
			-5				1				5				
AGG	AAC	AAG	ATC	AGC	AAA	GAR	TGC	CAG	CAG	GNG	TCC	GGA	GTG	TCC	136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	
	10					15					20				
CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTG	TTG	GTC	GAY	GAT	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	
	25					30					35				
CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	ARA	ACT	GGA	226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	
	40					45					50				
GTG	GCA	ACC	GAA	GCC	GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	GCC	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	
	55					60					65				
AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAR	GTG	GAC	AAG	ATC	GTG	316
Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val	
	70					75					80				
CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	TAT	361
Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr	
	85					90					95				
GAC	ACC	TTC	AAG	NNT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	CCT	406
Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro	
	100					105					110				
ATT	GAT	TAA	TTG	TTT	TGTA	TTT	GCT	GAA	TTTT	GACA	AA	AGG	TANTA		455
Ile	Asp	*													
	115														
TCG	TTAT	GNA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA							481

09076345-060701

- (2) INFORMATION FOR SEQ. ID NO: 45
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 2-2
- (ix) FEATURES
- (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
      -15                               -10

NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                               1           5

NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                               15           20

CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                               30           35

CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                               45           50

NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                               60           65

AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC     316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile
      70                               75           80

RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN     361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
      85                               90           95

TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN     406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
      100                              105          110

CCN RTT GAT TRA NYNNYYNNA YTNNGNNRRR NTTYRANAAT AAAGNNNTNTN     458
Pro Ile Asp *
      115

TNRTNNNRNA AAAAAAAAAA AAAAAA      484

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09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 46
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.2
 (ix) FEATURES
 (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCANRRNNN	AAR	ATG	AAR	YTN	CTC	TNN	TGY	YTN	RYN	TTY	NYC	RYY	46	
	Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala			
					-15						-10			
NTN	NTN	RTC	NNA	GYT	CAG	GCY	NTN	ACY	NAN	GNA	NAN	NTN	NAG	91
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	
		-5					1				5			
NNG	NNC	NAR	AYC	AGC	RNA	RAR	TGY	NAR	NNN	GNR	NNY	GGA	GTG	136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	
	10					15					20			
NAA	GAN	RYN	ATN	RNN	ARA	GYT	CGC	ANN	GGT	GNC	TNG	GNN	GAY	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	
	25					30					35			
CCY	AAA	NTG	AAR	NNN	CAN	NTY	YTY	TGC	NTN	NYN	ARG	RNN	YYY	226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	
	40					45					50			
NTR	GYN	RCN	GAA	NCN	GGA	GAN	RYN	RNN	GYN	GAN	RYR	YTN	ARR	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	
	55					60					65			
AAG	NTG	ANG	NRN	NNN	NNN	RNN	ANN	RNN	RAR	RAR	RYN	RRN	ARR	316
Lys	Leu	Lys	His	Val	Ala	Ser	Asn	Asp	Glu	Glu	Val	Asp	Lys	
	70					75					80			
NYN	NRN	ARN	NNN	NNN	NNN	NNG	ARN	RNN	NYN	NNN	RAR	RNR	NNN	361
Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	
	85					90					95			
TNN	RAN	NYN	YYN	AAN	NNN	NNY	NNN	RRN	ANN	ARN	CCN	RNN	TTY	406
Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	
	100					105					110			
CNN	RYT	RNT	TRN	NYNNNNNNN	YNNGNNRRR	NTTYRANAAT	AAAGNNNYTN							458
Pro	Ile	Asp	*											
	115													
TNRTNNNRNA	AAAAAAAAA	AAAAAA												484

- (2) INFORMATION FOR SEQ. ID NO: 48
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE:
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Genral Consensus of Clones,
B1, B2 and AFP-3

09876348.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
      Cys      Leu Ile Ser Leu Ile Leu Leu Val Ala Thr Val
                        Thr Leu Val
                        Val
-15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Tyr   Ile   Glu  Thr  Ala Asp Leu Glu Leu Leu Arg Lys  Gln Thr  Ala
      1                      5                      10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Lys   Lys  Asn Val      Ala      Glu Asp Ile Leu Thr Arg Ala
Ala      Thr      Ala      Ala      Val Ser      Lys  Asn
15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Asn Arg Asp Trp Glu      Arg Gln Leu Phe
Lys      Glu Glu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Ala Arg Arg Ala Ile Leu Val Ala Ala Ser      Glu Ile Glu
Ile Phe      Ala Leu Glu Ile Ile Asp      Val Val
      Leu      Asn      Glu Phe
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser *** Asp Glu
Ala Asp Thr Phe Arg Glu      Val Thr Arg Asn Thr Asn Asp Pro
Leu      His Ile Thr      Phe Arg Lys Glu      Ser Asp Asn
      65                      70                      75

Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro
Lys Ser Glu Asp Leu Ile Glu Asn Ala Thr      Glu Asp Val
      Thr      Ala      Thr
      80                      85                      90

Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro
Gln Asp Ser Val Phe Glu Val Thr      Val Val Leu Met  Asn Arg Ser
His      Ser Ala Asn Phe      His
95                      100                      105                      110

Asp Phe Ser Pro Ile Asp *** *** *
Asn   Phe Gly Asp Leu Phe Val *
Lys      Val
      115

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09875348-060701